

# EA2022-analytical-V3.R

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```
#=====
#Analytical statistics
#R Biostat Workshop IIUM
#Edre MA, DrPH
#=====
```

```
#objective 3: To determine the factors contributing to hypertension
#we want to know first what contributes to systolic hypertension
```

```
#Comparing numerical values: parametric
```

```
install.packages('readr')
```

```
## Error in install.packages : Updating loaded packages
```

```
library(readr)
hstat <- read_csv("healthstatus6.csv")
```

```
## Rows: 153 Columns: 17
## -- Column specification -----
## Delimiter: ","
## chr (3): sex, exercise, smoking
## dbl (14): id, age, wt, ht, sbp, dbp, hba1c, hcy, wt2, wt3, sbp2, sbp3, dbp2...
##
## i Use 'spec()' to retrieve the full column specification for this data.
## i Specify the column types or set 'show_col_types = FALSE' to quiet this message.
```

```
View(hstat)
```

```
#if our IV is categorical with 2 categories
#example, we want to know if being male has any relationship with sbp
#independent sample t test
```

```
install.packages("car") #testing for homogeneity of variance
```

```
## Error in install.packages : Updating loaded packages
```

```
library(car)
leveneTest(sbp ~ sex, data = hstat, center=mean)

## Warning in leveneTest.default(y = y, group = group, ...): group coerced to
## factor.

## Levene's Test for Homogeneity of Variance (center = mean)
##      Df F value Pr(>F)
## group 1  0.5477 0.4604
##      151
```

```
t.test(sbp ~ sex, data = hstat)
```

```
##
## Welch Two Sample t-test
##
## data: sbp by sex
## t = 0.4972, df = 141.8, p-value = 0.6198
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.928972  3.225357
## sample estimates:
## mean in group Female    mean in group Male
##          132.6000          131.9518
```

```
#we want to visualize the comparison
```

```
install.packages("ggplot2")
```

```
## Error in install.packages : Updating loaded packages
```

```
library(ggplot2)
install.packages("ggpubr")
```

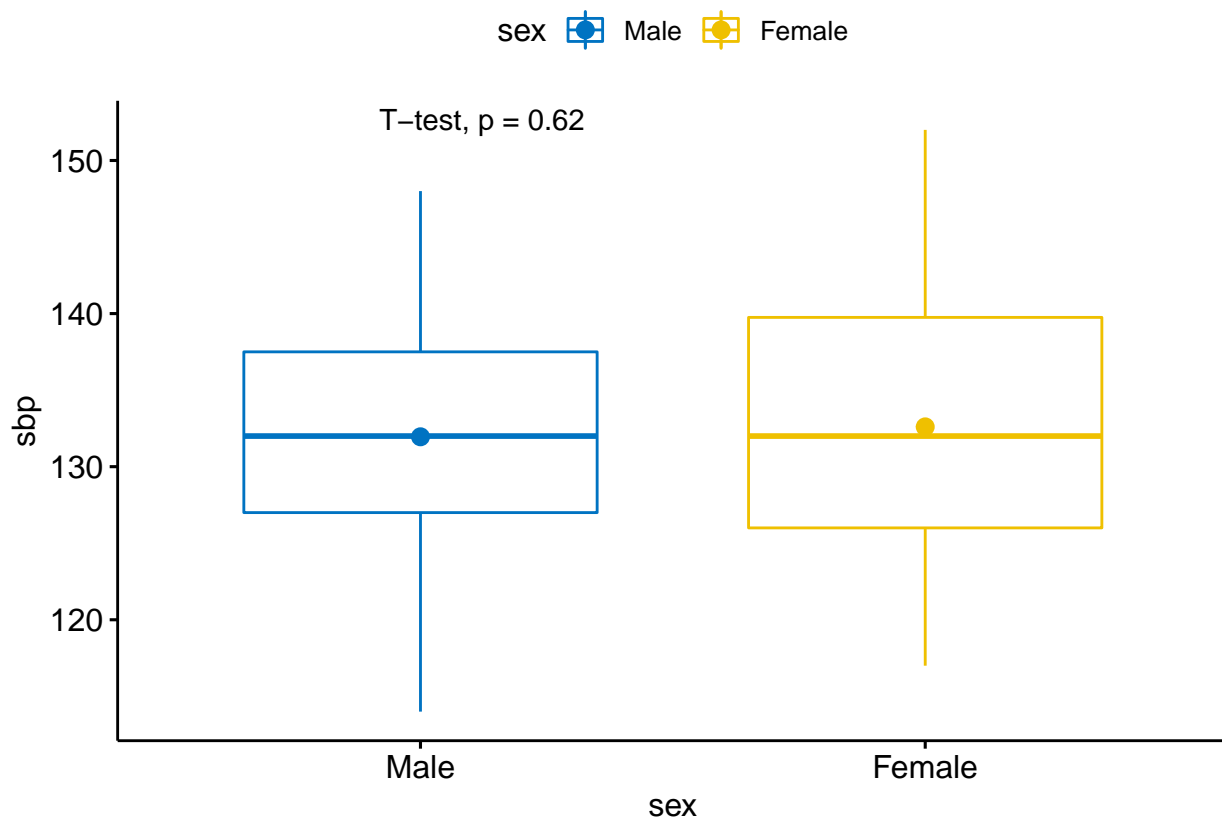
```
## Error in install.packages : Updating loaded packages
```

```
library(ggpubr)
ggboxplot(hstat, x = "sex", y = "sbp",
          color = "sex",
          palette = "jco",
          add = "mean") +
  stat_compare_means(method = "t.test")
```

```
## Warning: 'fun.y' is deprecated. Use 'fun' instead.
```

```
## Warning: 'fun.ymin' is deprecated. Use 'fun.min' instead.
```

```
## Warning: 'fun.ymax' is deprecated. Use 'fun.max' instead.
```



*#now we know sex has no effect on sbp in our study*  
*#we want to know now, does exercise have an effect (low,mod,high intensity)*  
*#one way ANOVA*

```
install.packages("psych")
```

```
## Error in install.packages : Updating loaded packages
```

```
library(psych)
describe.by(hstat$sbp, hstat$exercise)
```

```
## Warning: describe.by is deprecated. Please use the describeBy function
```

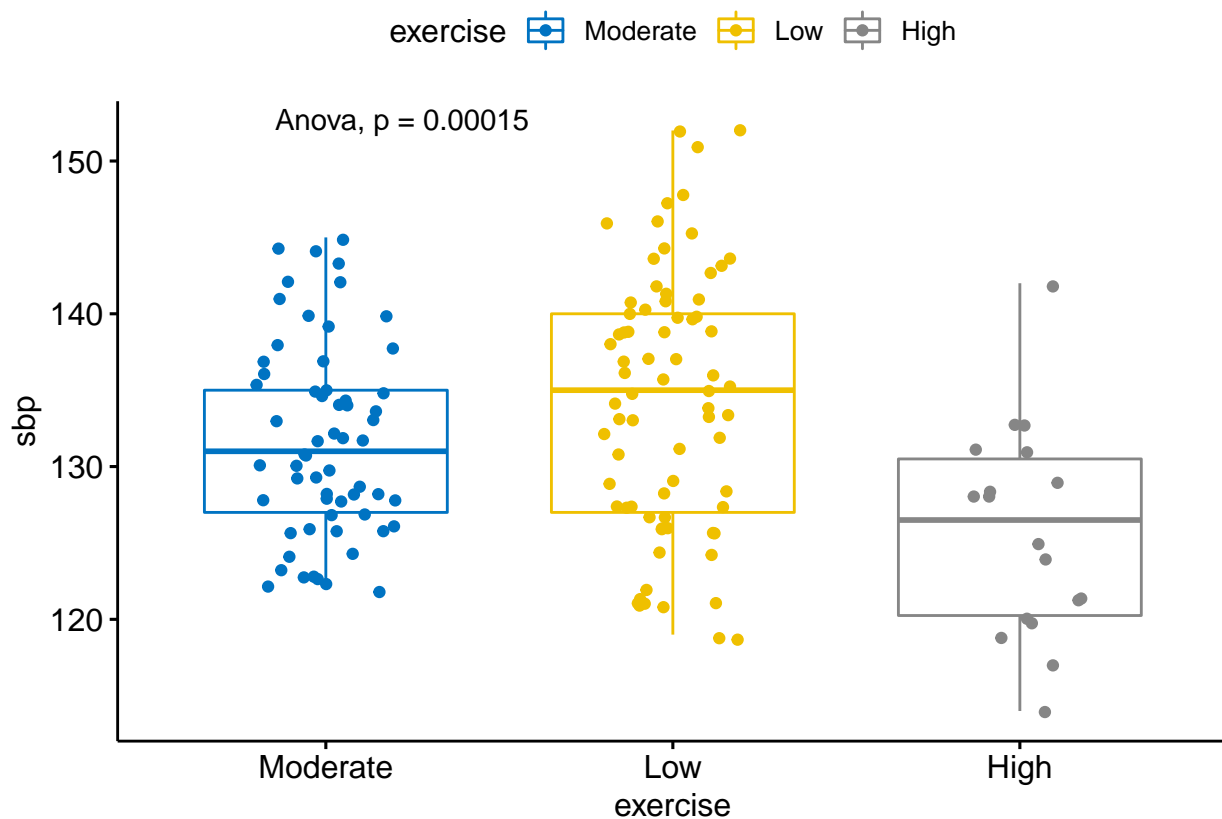
```
##
## Descriptive statistics by group
## group: High
## vars n mean sd median trimmed mad min max range skew kurtosis se
## X1 1 18 125.78 6.97 126.5 125.5 8.15 114 142 28 0.35 -0.48 1.64
## -----
## group: Low
## vars n mean sd median trimmed mad min max range skew kurtosis se
## X1 1 74 134.24 8.57 135 134.15 10.38 119 152 33 0.03 -0.92 1
## -----
## group: Moderate
```

```
##      vars  n   mean    sd median trimmed  mad min max range skew kurtosis  se
## X1      1 61 131.74 6.28    131  131.45 5.93 122 145    23 0.33   -0.84 0.8
```

```
one.way = aov(sbp ~ exercise, data = hstat)
summary(one.way)
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## exercise      2   1064    532.0    9.324 0.000152 ***
## Residuals    150    8559     57.1
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ggboxplot(hstat, x = "exercise", y = "sbp",
           color = "exercise",
           palette = "jco",
           add = "jitter") +
  stat_compare_means(method = "anova")
```



```
#yes, there is significant effect of exercise on sbp
#but, which pair comparison has most effect?
```

```
leveneTest(sbp ~ exercise, data = hstat, center=mean)
```

```
## Warning in leveneTest.default(y = y, group = group, ...): group coerced to
## factor.
```

```

## Levene's Test for Homogeneity of Variance (center = mean)
##      Df F value Pr(>F)
## group  2  4.2458 0.01608 *
##      150
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#significant p value, thus equal variance not assumed
#use Welch one way ANOVA

oneway.test(sbp ~ exercise, data = hstat) #for overall significance

##
## One-way analysis of means (not assuming equal variances)
##
## data:  sbp and exercise
## F = 9.5994, num df = 2.000, denom df = 48.988, p-value = 0.0003037

pairwise.t.test(hstat$sbp, hstat$exercise,
                 p.adjust.method = "BH", pool.sd = FALSE)

##
## Pairwise comparisons using t tests with non-pooled SD
##
## data:  hstat$sbp and hstat$exercise
##
##           High      Low
## Low      0.00035 -
## Moderate 0.00470 0.05254
##
## P value adjustment method: BH

#if equal variance assumed, use Tukey
tukey.one.way<-TukeyHSD(one.way)
tukey.one.way

## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = sbp ~ exercise, data = hstat)
##
## $exercise
##           diff      lwr      upr      p adj
## Low-High      8.465465  3.766172 13.1647594 0.0001043
## Moderate-High  5.959927  1.163662 10.7561923 0.0105140
## Moderate-Low -2.505538 -5.597805  0.5867282 0.1371181

#Exercise adds benefit in sbp reduction
#does it correlate with weight?

#pearson correlation coefficient test

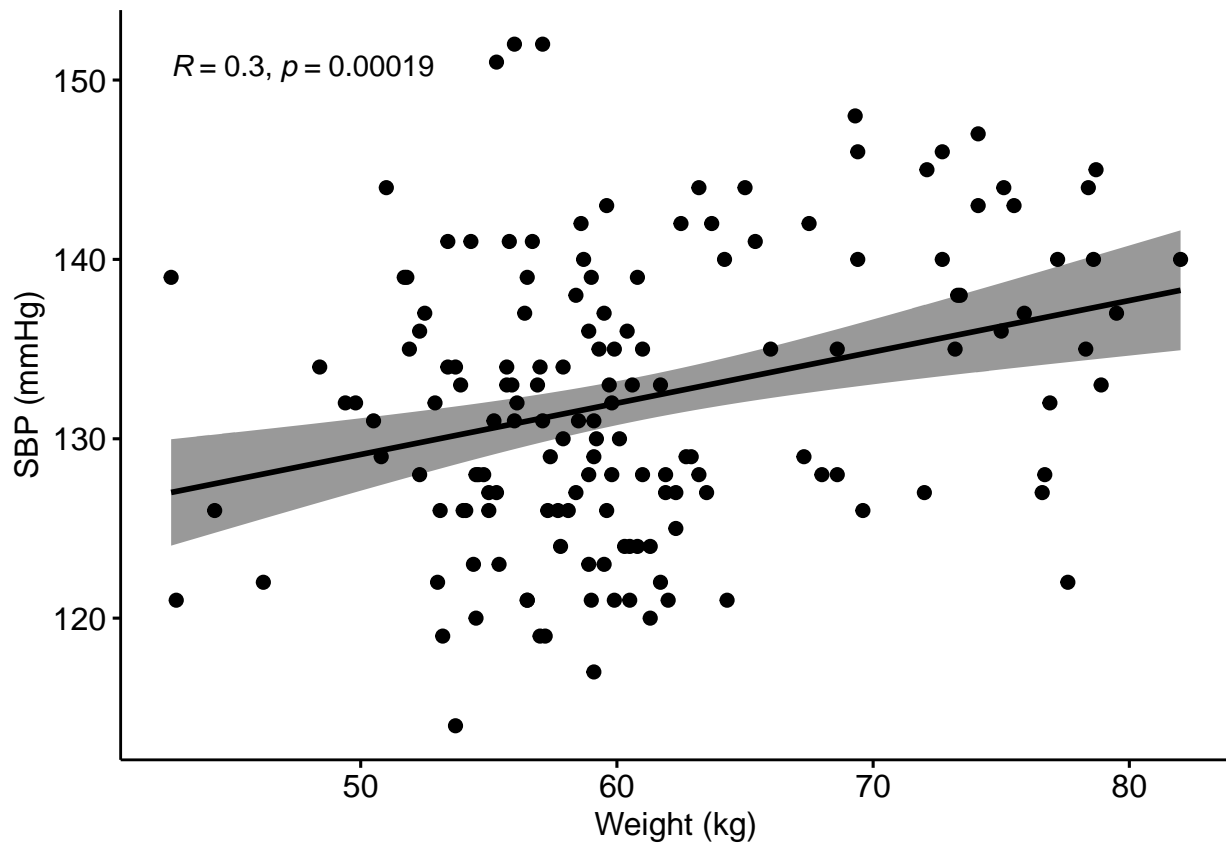
cor.test(hstat$wt,hstat$sbp, method="pearson")

```

```
##
## Pearson's product-moment correlation
##
## data: hstat$wt and hstat$sbp
## t = 3.8267, df = 151, p-value = 0.0001897
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.1455186 0.4354641
## sample estimates:
## cor
## 0.2973312
```

```
ggscatter(hstat, x = "wt", y = "sbp",
  add = "reg.line",
  conf.int = TRUE,
  cor.coef = TRUE,
  cor.method = "pearson",
  xlab = "Weight (kg)", ylab = "SBP (mmHg)")
```

```
## 'geom_smooth()' using formula 'y ~ x'
```



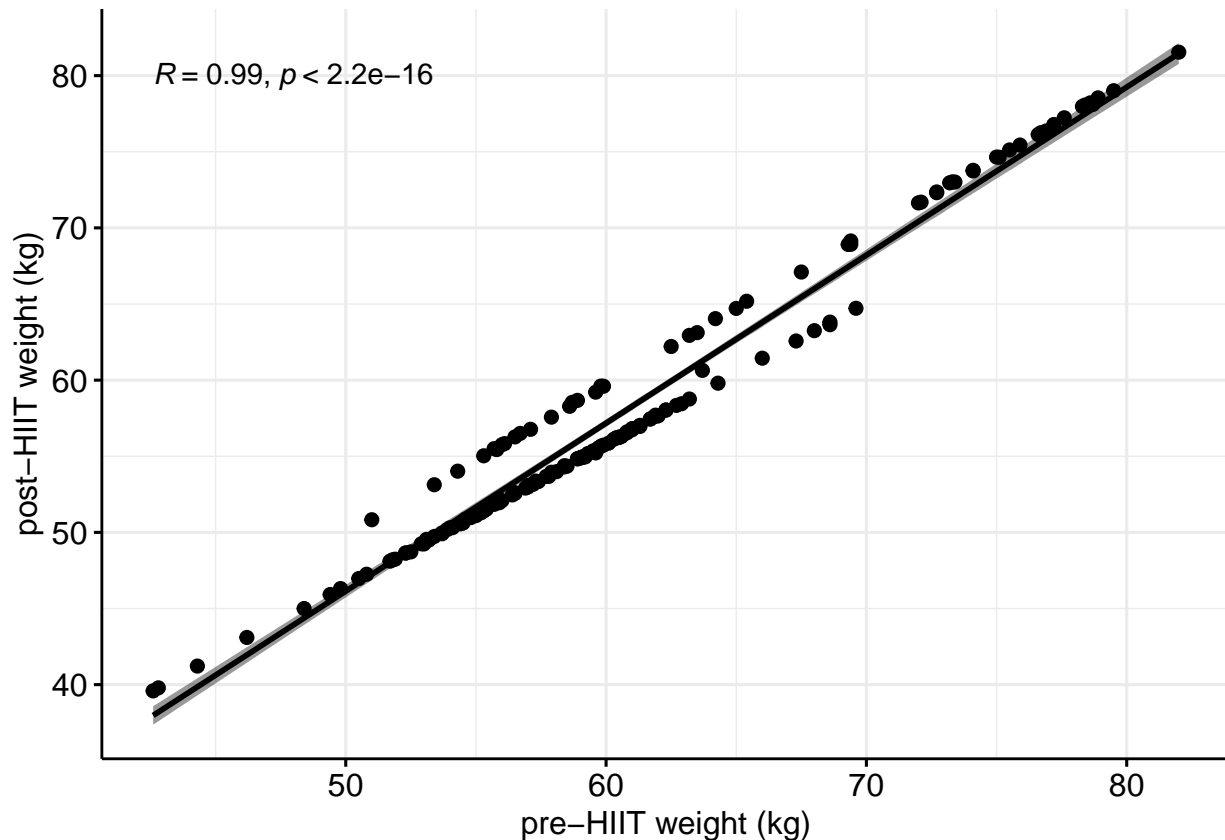
```
#yes, the heavier the person, the higher the sbp
#now you conducted a high-intensity interval training (HIIT) intervention
#you want to measure pre and post HIIT effect on weight
#paired t test
```

```
t.test(hstat$wt, hstat$wt2, paired=TRUE)
```

```
##  
## Paired t-test  
##  
## data: hstat$wt and hstat$wt2  
## t = 19.015, df = 152, p-value < 2.2e-16  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## 2.445299 3.012348  
## sample estimates:  
## mean of the differences  
## 2.728824
```

```
ggscatter(hstat, x = "wt", y = "wt2",  
          add = "reg.line",  
          conf.int = TRUE,  
          cor.coef = TRUE,  
          cor.method = "pearson",  
          xlab = "pre-HIIT weight (kg)", ylab = "post-HIIT weight (kg)") +  
  grids(linetype = "solid")
```

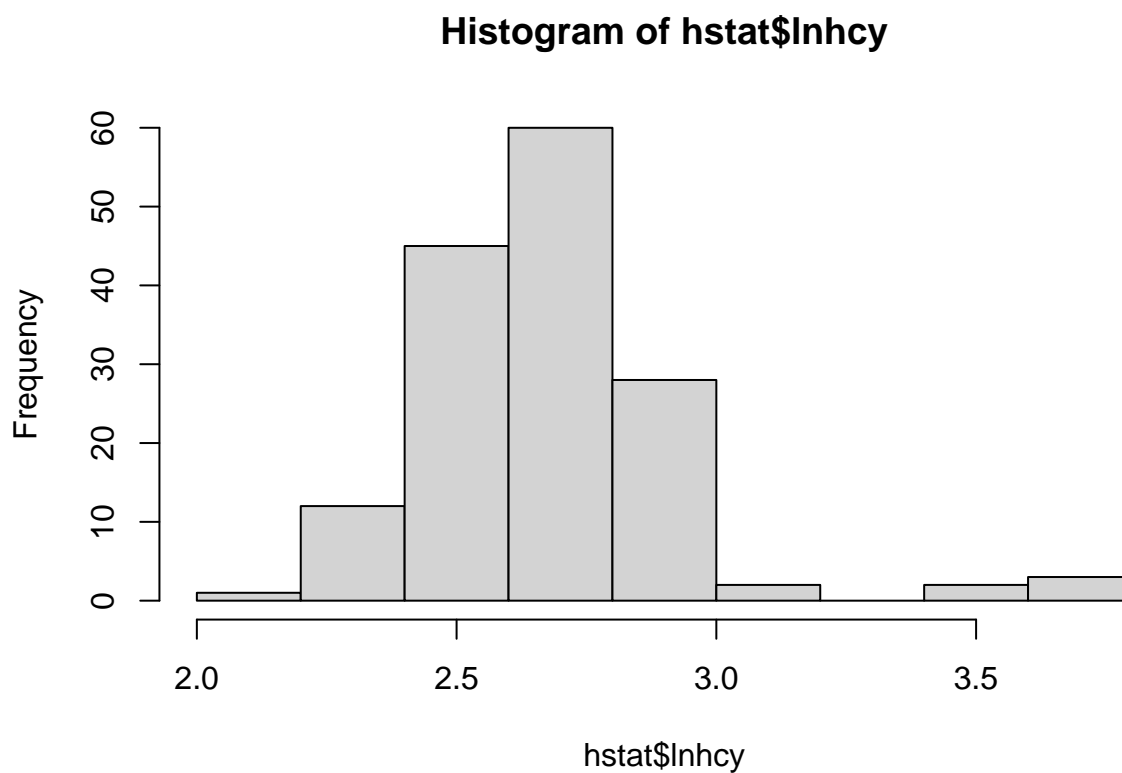
```
## 'geom_smooth()' using formula 'y ~ x'
```



```
#Now we know that sbp is affected by weight.  
#exercise gives additional benefit to weight reduction  
#you are now concerned with the exercise giving effect on cardiovascular health  
#homocysteine (hcy) relates to cardiovascular health from literature  
#what are the factors contributing to hcy level?
```

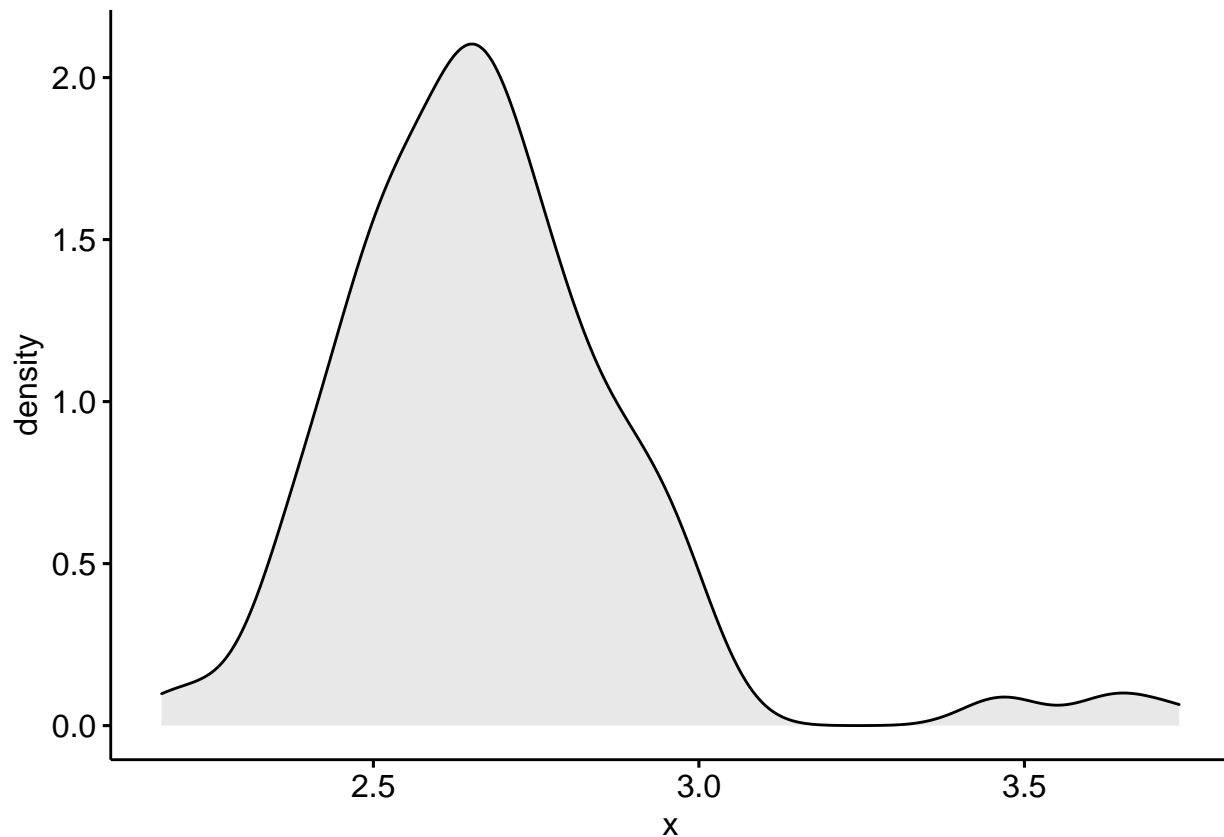
```
#comparing numerical values: non-parametric
```

```
#try transforming data into normal distribution by ln  
hstat$lnhcy= log(hstat$hcy)  
hist(hstat$lnhcy)
```



```
ggdensity(hstat$lnhcy, fill = "lightgray")
```





```
#still not normally distributed
#need to do non-parametric test
```

```
#female has higher or lower hcy level compared to male?
#mann whitney U test
```

```
install.packages("SmartEDA")
```

```
## Warning in install.packages :
##   package 'SmartEDA' is in use and will not be installed
```

```
library(SmartEDA)
ExpCustomStat(hstat,
  Cvar="sex",
  Nvar="hcy",
  stat=c("median","IQR"),
  gpby=TRUE,
  dcast=F)
```

```
##      sex Attribute median  IQR
## 1:  Male      hcy   14.3 3.650
## 2: Female      hcy   14.1 3.575
```

```
wilcox.test(hcy~sex, data=hstat) #synonym to Mann Whitney U test
```

```
##  
## Wilcoxon rank sum test with continuity correction  
##  
## data: hcy by sex  
## W = 2658.5, p-value = 0.3675  
## alternative hypothesis: true location shift is not equal to 0
```

```
#sex has no signififant relationship with hcy
```

```
#how about exercise intensity?  
#kruskal wallis test
```

```
ExpCustomStat(hstat,  
               Cvar="exercise",  
               Nvar="hcy",  
               stat=c("median","IQR"),  
               gpby=TRUE,  
               dcast=F)
```

```
##      exercise Attribute median   IQR  
## 1: Moderate      hcy  14.30 2.600  
## 2:      Low      hcy  14.55 5.075  
## 3:      High      hcy  12.35 2.350
```

```
kruskal.test(hcy ~ exercise, data = hstat) #if significant, proceed with pairwise comparison
```

```
##  
## Kruskal-Wallis rank sum test  
##  
## data: hcy by exercise  
## Kruskal-Wallis chi-squared = 11.436, df = 2, p-value = 0.003286
```

```
pairwise.wilcox.test(hstat$hcy, hstat$exercise,p.adjust.method = "BH")
```

```
##  
## Pairwise comparisons using Wilcoxon rank sum test with continuity correction  
##  
## data: hstat$hcy and hstat$exercise  
##  
##           High Low  
## Low      0.005 -  
## Moderate 0.014 0.133  
##  
## P value adjustment method: BH
```

```
#high intensity exercise significantly gives lower HCY compared to low/mod  
#you proceed in continuing the HIIT intervention as it gives benefit to both sbp and hcy
```

```
#measure effectiveness again on weight reduction  
#wilcoxon signed rank test
```

```
wilcox.test(hstat$wt,hstat$wt2,paired=TRUE)
```

```
##  
## Wilcoxon signed rank test with continuity correction  
##  
## data: hstat$wt and hstat$wt2  
## V = 11781, p-value < 2.2e-16  
## alternative hypothesis: true location shift is not equal to 0
```

```
#yes, the HIIT is effective in weight reduction  
#however you noticed some of your respondents are diabetic  
#worry that your intervention gives more harm than good  
#finding relationship between hba1c and both sbp/hcy  
#spearman correlation coefficient test
```

```
cor.test(hstat$hba1c,hstat$sbp, method="spearman")
```

```
## Warning in cor.test.default(hstat$hba1c, hstat$sbp, method = "spearman"):  
## Cannot compute exact p-value with ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data: hstat$hba1c and hstat$sbp  
## S = 416312, p-value = 0.0001441  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## 0.3025482
```

```
cor.test(hstat$hba1c,hstat$hcy, method="spearman")
```

```
## Warning in cor.test.default(hstat$hba1c, hstat$hcy, method = "spearman"):  
## Cannot compute exact p-value with ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data: hstat$hba1c and hstat$hcy  
## S = 515097, p-value = 0.09116  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## 0.1370514
```

```
#you conclude that only sbp has a significant correlation with hba1c  
#in future, you would prioritize  
#giving HITT intervention to the diabetic & hypertensive patients
```

```
#now, you are focused back to your objective 3  
#factors contributing to hypertension (hpt)
```

```
#comparing categorical variables
```

```
install.packages("dplyr")
```

```
## Warning in install.packages :  
## package 'dplyr' is in use and will not be installed
```

```
library(dplyr)
```

```
hstat2<-hstat %>%  
  mutate(hpt=if_else(hstat$sbp<140 & hstat$dbp<90,'normal','high'))  
View(hstat2)
```

```
#smoking has a relationship with hpt?  
#chi square test
```

```
chisq.test(hstat2$hpt,hstat2$smoking,correct=F)
```

```
##  
## Pearson's Chi-squared test  
##  
## data: hstat2$hpt and hstat2$smoking  
## X-squared = 15.607, df = 1, p-value = 7.797e-05
```

```
chisq.test(hstat2$hpt,hstat2$smoking)$observed
```

```
##           hstat2$smoking  
## hstat2$hpt No Yes  
##    high    23  36  
##   normal   67  27
```

```
#yes, smoking is significantly related to hpt. More smokers are hypertensive
```

```
#how about BMI status and hpt?
```

```
hstat3<- hstat2 %>%  
  mutate(height_m = ht / 100,bmi = wt / (height_m^2))  
View(hstat3)  
hstat3$bmistatus<- cut(hstat3$bmi,  
                       breaks=c(-Inf, 18.49999, 24.9999, 29.9999, Inf),  
                       labels=c("underweight", "normal", "overweight", "obese"))
```

```
#fisher's exact test (used when more than 20% celss with expected count less than 5)  
chisq.test(hstat3$hpt,hstat3$bmistatus)$expected
```

```
## Warning in chisq.test(hstat3$hpt, hstat3$bmistatus): Chi-squared approximation
## may be incorrect
```

```
##           hstat3$bmistatus
## hstat3$hpt underweight   normal overweight   obese
##      high      2.313725 28.92157    18.5098  9.254902
##      normal    3.686275 46.07843    29.4902 14.745098
```

```
fisher.test(hstat3$hpt, hstat3$bmistatus)
```

```
##
## Fisher's Exact Test for Count Data
##
## data:  hstat3$hpt and hstat3$bmistatus
## p-value = 1.205e-05
## alternative hypothesis: two.sided
```

```
#significant relationship between hpt and bmi status
```

```
#reporting your findings in table form
```

```
#package needed
"sjPlot"
"apaTables"
```

```
install.packages("sjPlot")
```

```
## Error in install.packages : Updating loaded packages
```

```
library(sjPlot)
install.packages("apaTables")
```

```
## Error in install.packages : Updating loaded packages
```

```
library(apaTables)
```

```
#table created in word file in your directory!
#sjt.xtab(hstat3$smoking, hstat3$hpt, file = "sjt_contingency.doc")
#apa.aov.table(one.way, filename="Table_anova.doc", table.number = 2)
```